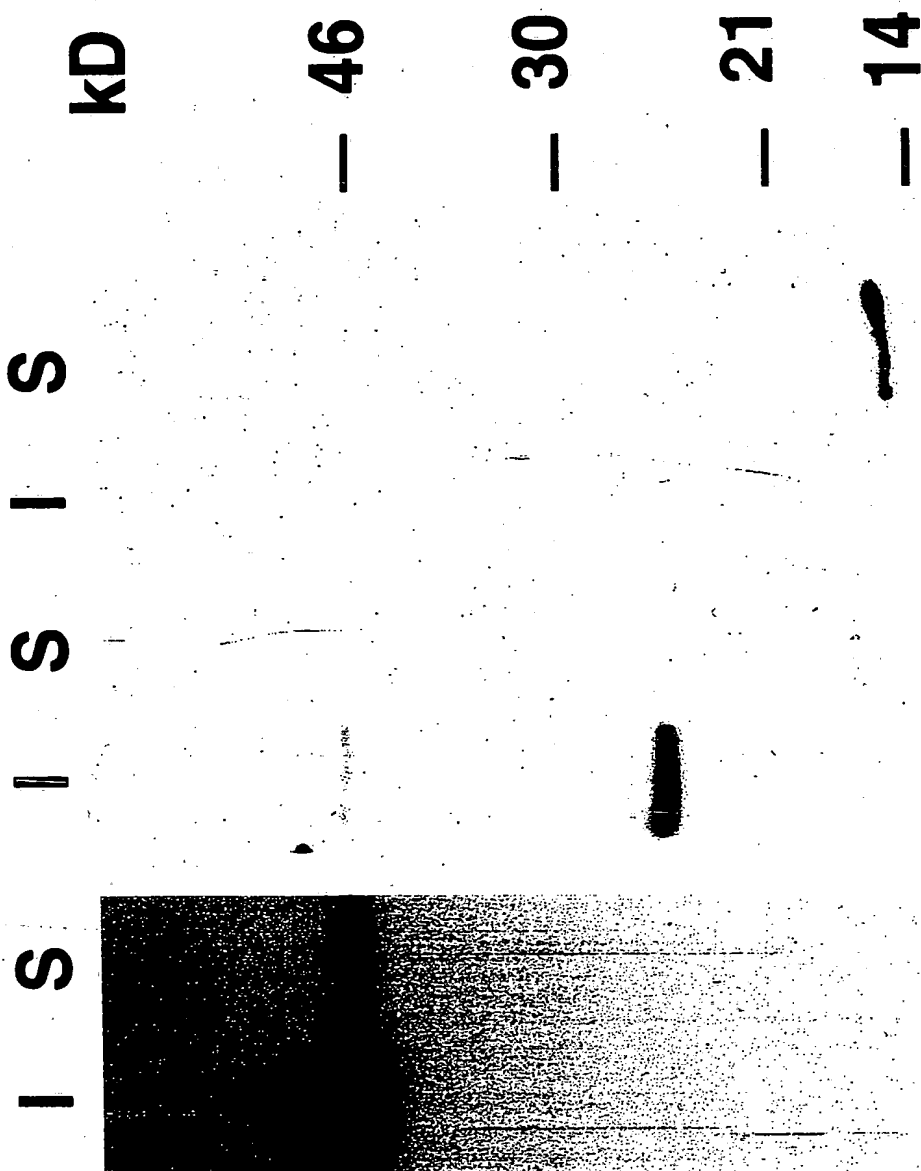


IncA/mycHIS IncB/mycHIS IncB Δ hydro
/mycHIS



Figur 1

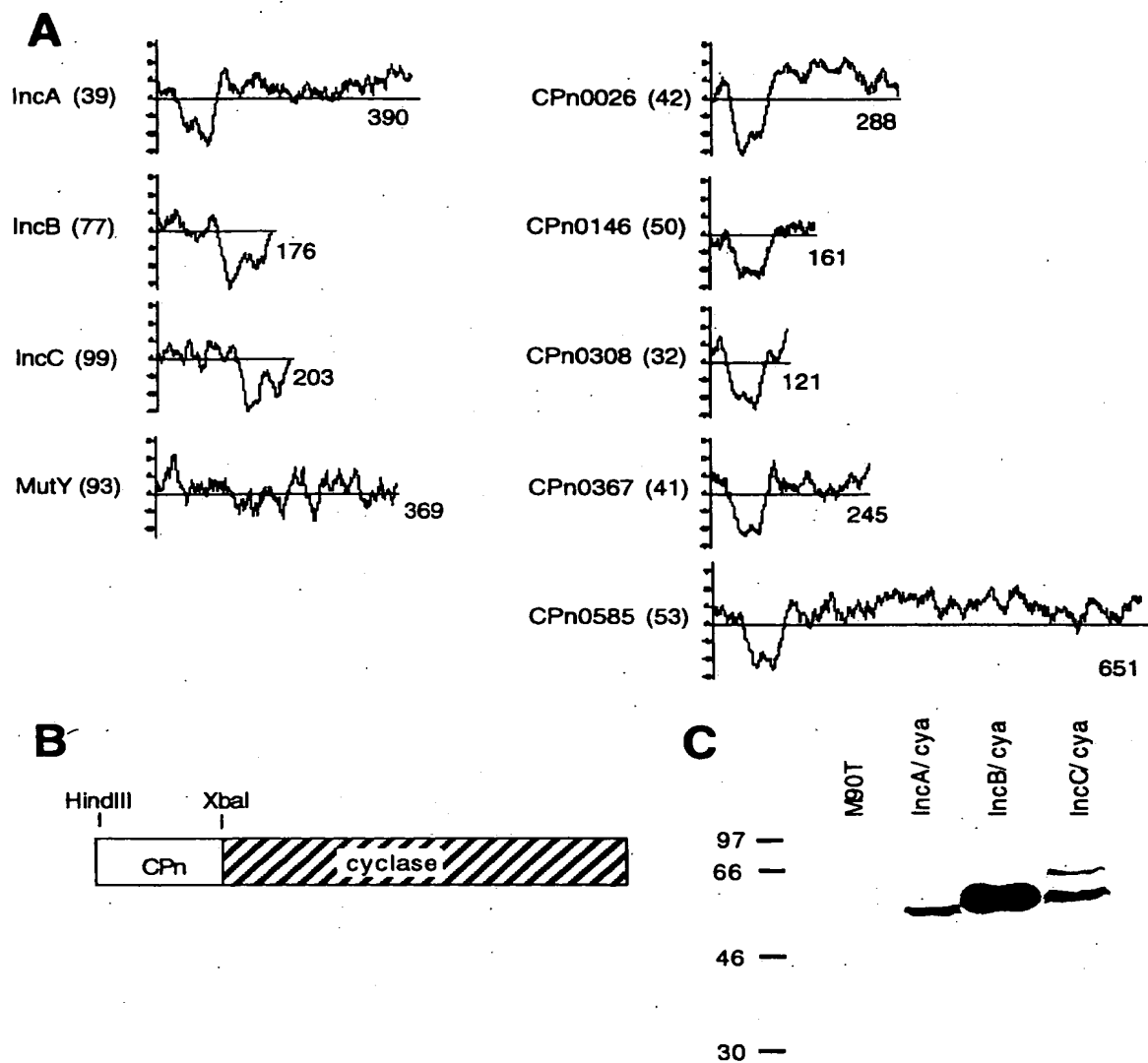


Figure 2

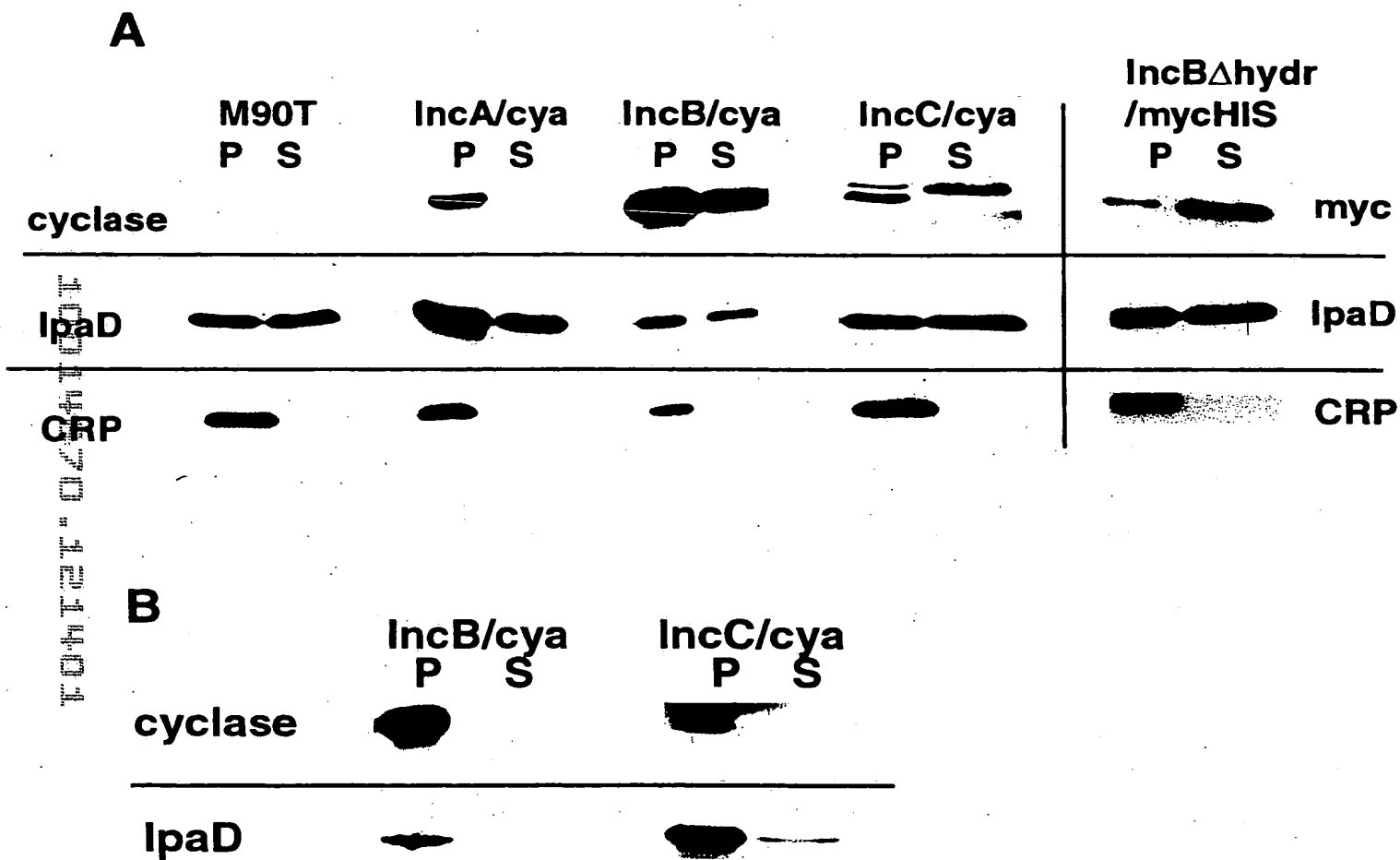


Figure 3

IncC/cya IncA/cya MutY/cya

P S P S P S



cyclase



IpaD



CRP

Figure 4



Figure 5

Figure 1: Full-length Sequence of *C. pneumoniae* 76kDa Gene.

ataaaatctt taaaacagg ctgcattaa ttattagtga gagctttttt tttatttttt 60

ataataaaac taaaagattt ttattatttt ttgagttttt atg gtt aat cct att 115
Met Val Asn Pro Ile
1 5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt 163
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu
10 15 20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct 211
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala
25 30 35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat 259
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp
40 45 50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg 307
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met
55 60 65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct 355
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser
70 75 80 85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg 403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr
90 95 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct 451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala
105 110 115

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct 499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala
120 125 130

ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct 547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala
135 140 145

act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc 595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala
150 155 160 165

gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct 643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala
170 175 180

tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc 691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe
185 190 195

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Figure 1 (continued)

gac	ctc	tta	cag	gct	gct	ctt	ctc	caa	tct	gta	gca	aac	aat	aac	aaa	739
Asp	Leu	Leu	Gln	Ala	Ala	Leu	Leu	Gln	Ser	Val	Ala	Asn	Asn	Asn	Lys	
		200					205					210				
gca	gct	gag	ctt	ctt	aaa	gag	atg	caa	gat	aac	cca	gta	gtc	cca	ggg	787
Ala	Ala	Glu	Leu	Leu	Lys	Glu	Met	Gln	Asp	Asn	Pro	Val	Val	Pro	Gly	
	215				220					225						
aaa	acg	cct	gca	att	gct	caa	tct	tta	gtt	gat	cag	aca	gat	gct	aca	835
Lys	Thr	Pro	Ala	Ile	Ala	Gln	Ser	Leu	Val	Asp	Gln	Thr	Asp	Ala	Thr	
230					235					240					245	
gcg	aca	cag	ata	gag	aaa	gat	gga	aat	gcg	att	agg	gat	gca	tat	ttt	883
Ala	Thr	Gln	Ile	Glu	Lys	Asp	Gly	Asn	Ala	Ile	Arg	Asp	Ala	Tyr	Phe	
			250					255						260		
gca	gga	cag	aac	gct	agt	gga	gct	gta	gaa	aat	gct	aaa	tct	aat	aac	931
Ala	Gly	Gln	Asn	Ala	Ser	Gly	Ala	Val	Glu	Asn	Ala	Lys	Ser	Asn	Asn	
		265					270					275				
agt	ata	agc	aac	ata	gat	tca	gct	aaa	gca	gca	atc	gct	act	gct	aag	979
Ser	Ile	Ser	Asn	Ile	Asp	Ser	Ala	Lys	Ala	Ala	Ile	Ala	Thr	Ala	Lys	
	280					285					290					
aca	caa	ata	gct	gaa	gct	cag	aaa	aag	ttc	ccc	gac	tct	cca	att	ctt	1027
Thr	Gln	Ile	Ala	Glu	Ala	Gln	Lys	Lys	Phe	Pro	Asp	Ser	Pro	Ile	Leu	
	295					300				305						
caa	gaa	gcg	gaa	caa	atg	gta	ata	cag	gct	gag	aaa	gat	ctt	aaa	aat	1075
Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	Lys	Asp	Leu	Lys	Asn	
310					315					320					325	
atc	aaa	cct	gca	gat	ggg	tct	gat	gtt	cca	aat	cca	gga	act	aca	gtt	1123
Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	Pro	Gly	Thr	Thr	Val	
			330					335						340		
gga	ggc	tcc	aag	caa	caa	gga	agt	agt	att	ggg	agt	att	cgt	gtt	tcc	1171
Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	Ser	Ile	Arg	Val	Ser	
		345					350						355			
atg	ctg	tta	gat	gat	gct	gaa	aat	gag	acc	gct	tcc	att	ttg	atg	tct	1219
Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	Ser	Ile	Leu	Met	Ser	
		360					365					370				
ggg	ttt	cgt	cag	atg	att	cac	atg	ttc	aat	acg	gaa	aat	cct	gat	tct	1267
Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	Glu	Asn	Pro	Asp	Ser	
	375					380					385					
caa	gct	gcc	caa	cag	gag	ctc	gca	gca	caa	gct	aga	gca	gcg	aaa	gcc	1315
Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	Arg	Ala	Ala	Lys	Ala	
390					395					400					405	
gct	gga	gat	gac	agt	gct	gct	gca	gcg	ctg	gca	gat	gct	cag	aaa	gct	1363
Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Asp	Ala	Gln	Lys	Ala	
				410					415						420	

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Figure 1 (continuation)

tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat	1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn	
425 430 435	
gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct	1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro	
440 445 450	
ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag	1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys	
455 460 465	
acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt	1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly	
470 475 480 485	
tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat	1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn	
490 495 500	
gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca	1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr	
505 510 515	
cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca	1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr	
520 525 530	
gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga	1747
Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly	
535 540 545	
gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc	1795
Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile	
550 555 560 565	
cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca	1843
Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr	
570 575 580	
tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt	1891
Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu	
585 590 595	
tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt	1939
Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe	
600 605 610	
gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa	1987
Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu	
615 620 625	
acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta	2035
Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu	
630 635 640 645	

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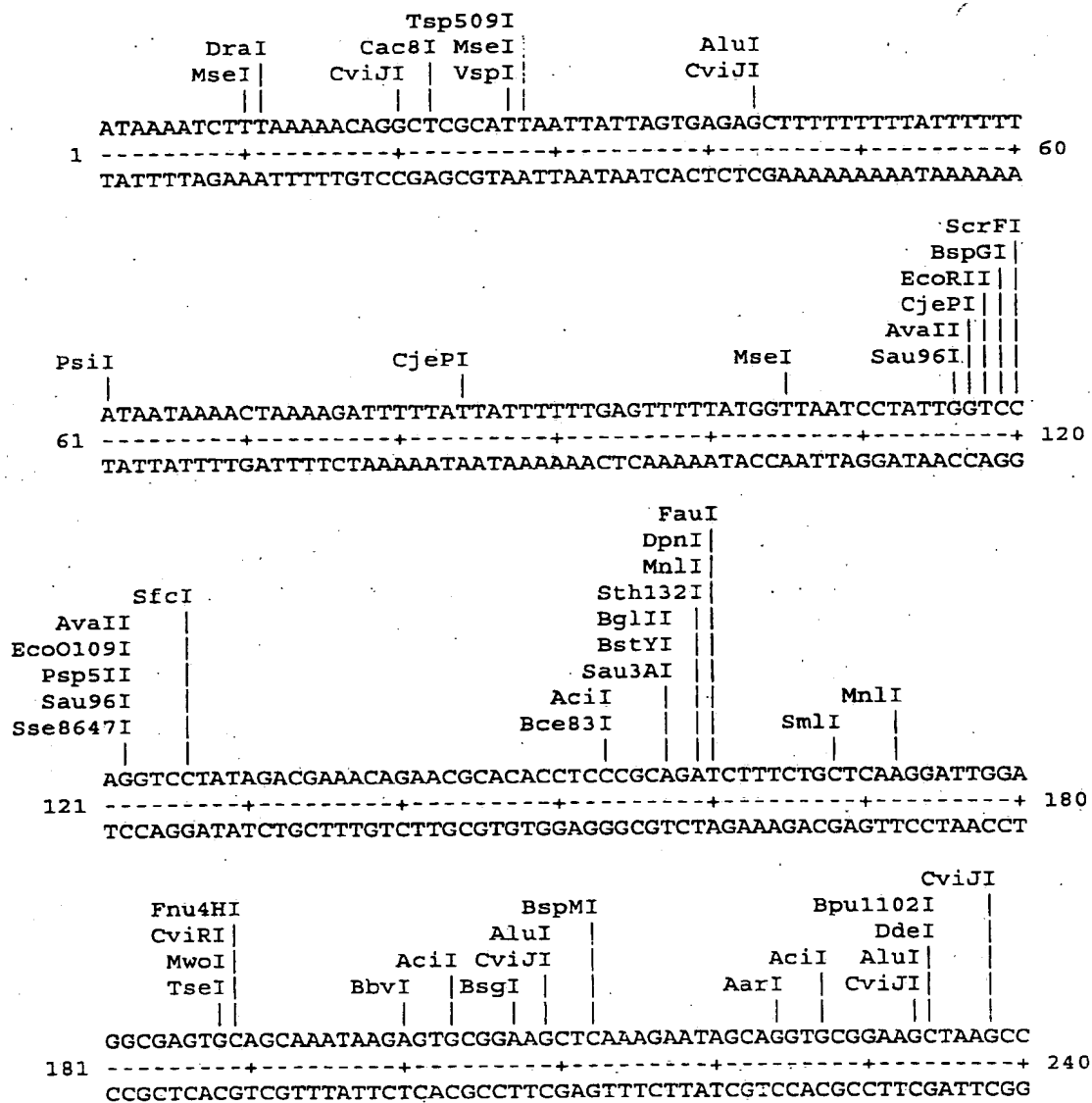
Figure 1 (continued)

tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga 2083
Tyr Ser Gly Tyr Leu Gln
650

ttattatgtg ctttggttaag gcctttgttg aggccttacc aacacactag aacgatcttc 2143

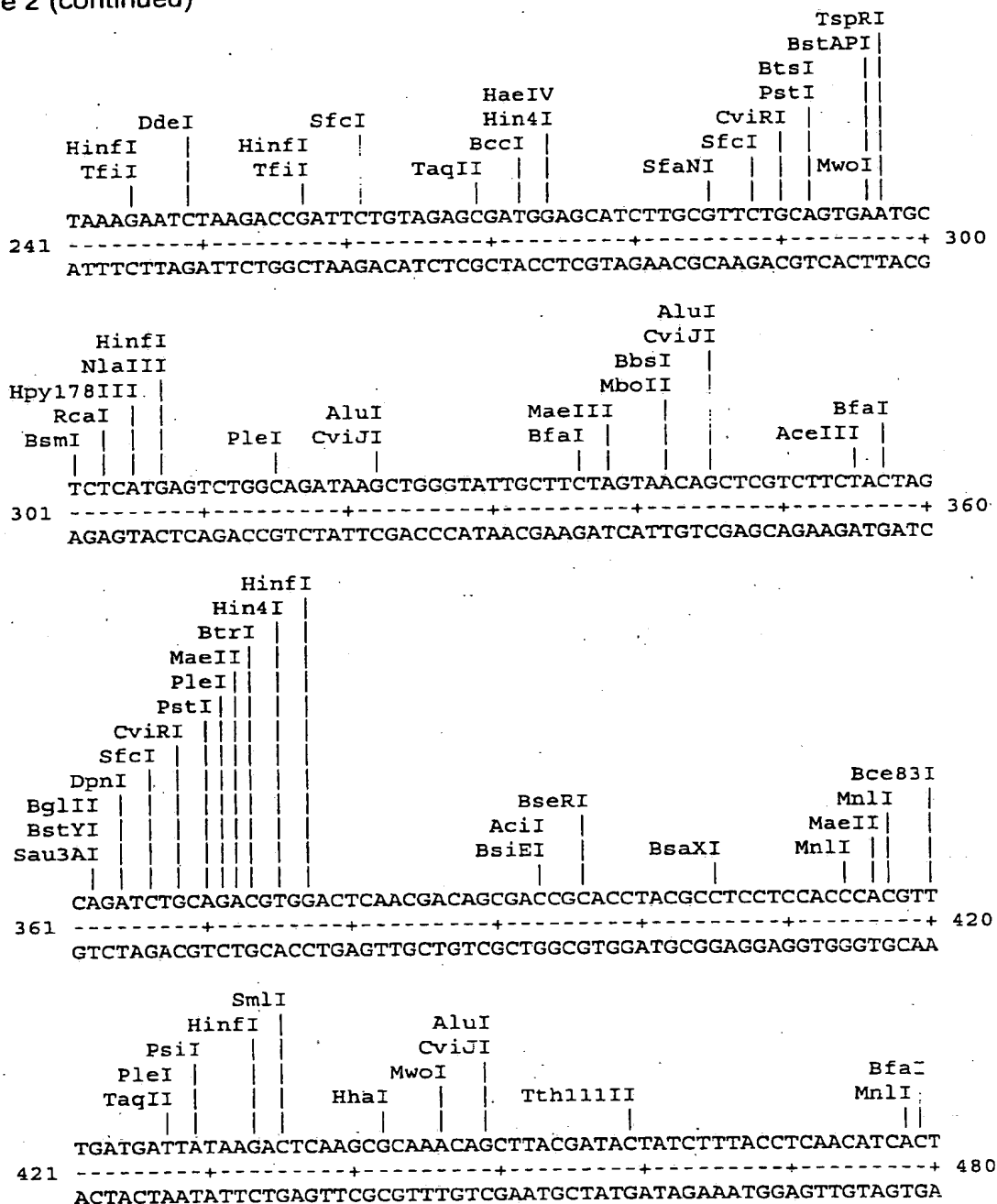
aataaataaa aga 2156

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Figure 2: Restriction enzyme map of *C. pneumoniae* 76kDa gene.

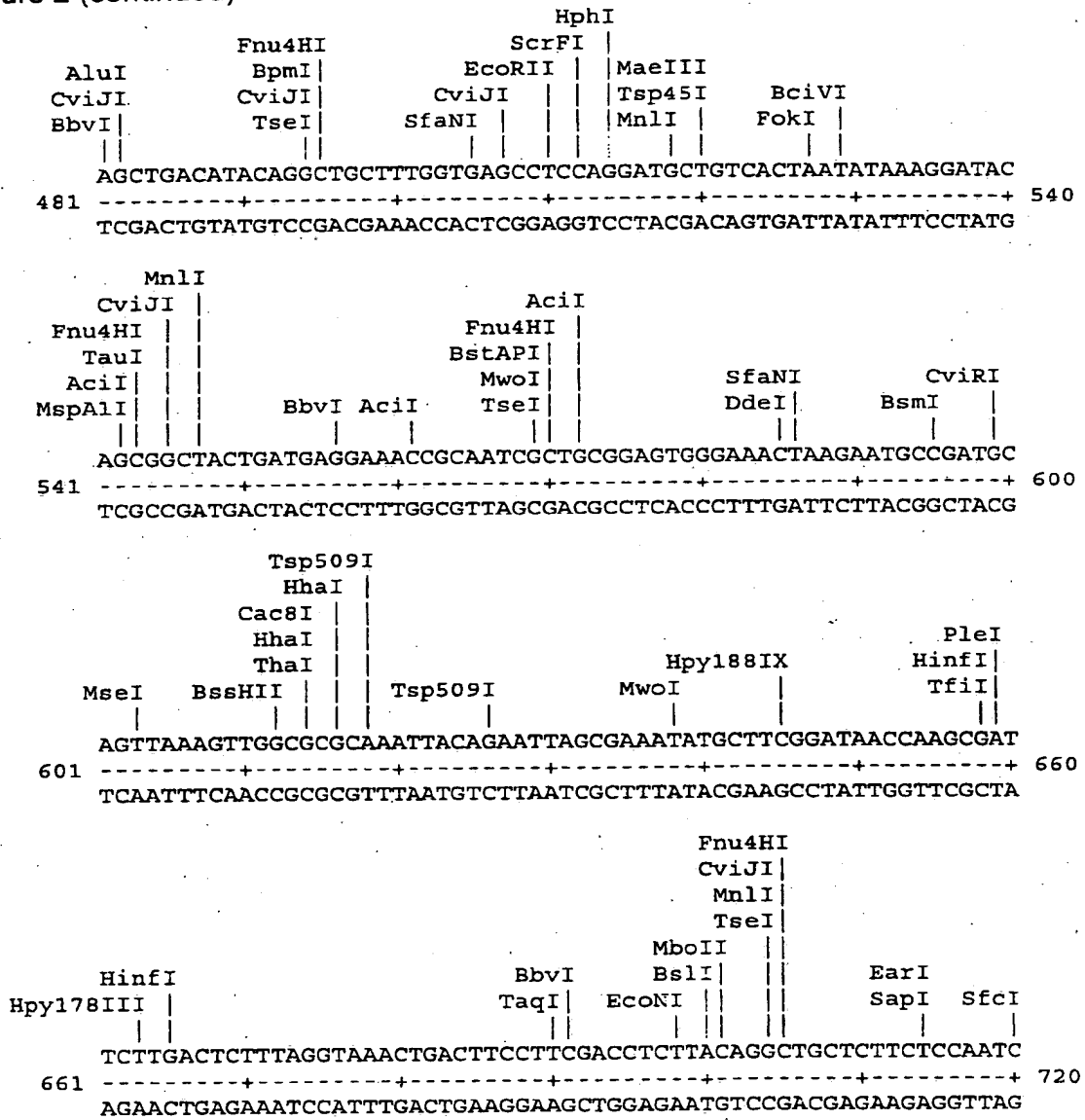
10014570-121401

Figure 2 (continued)



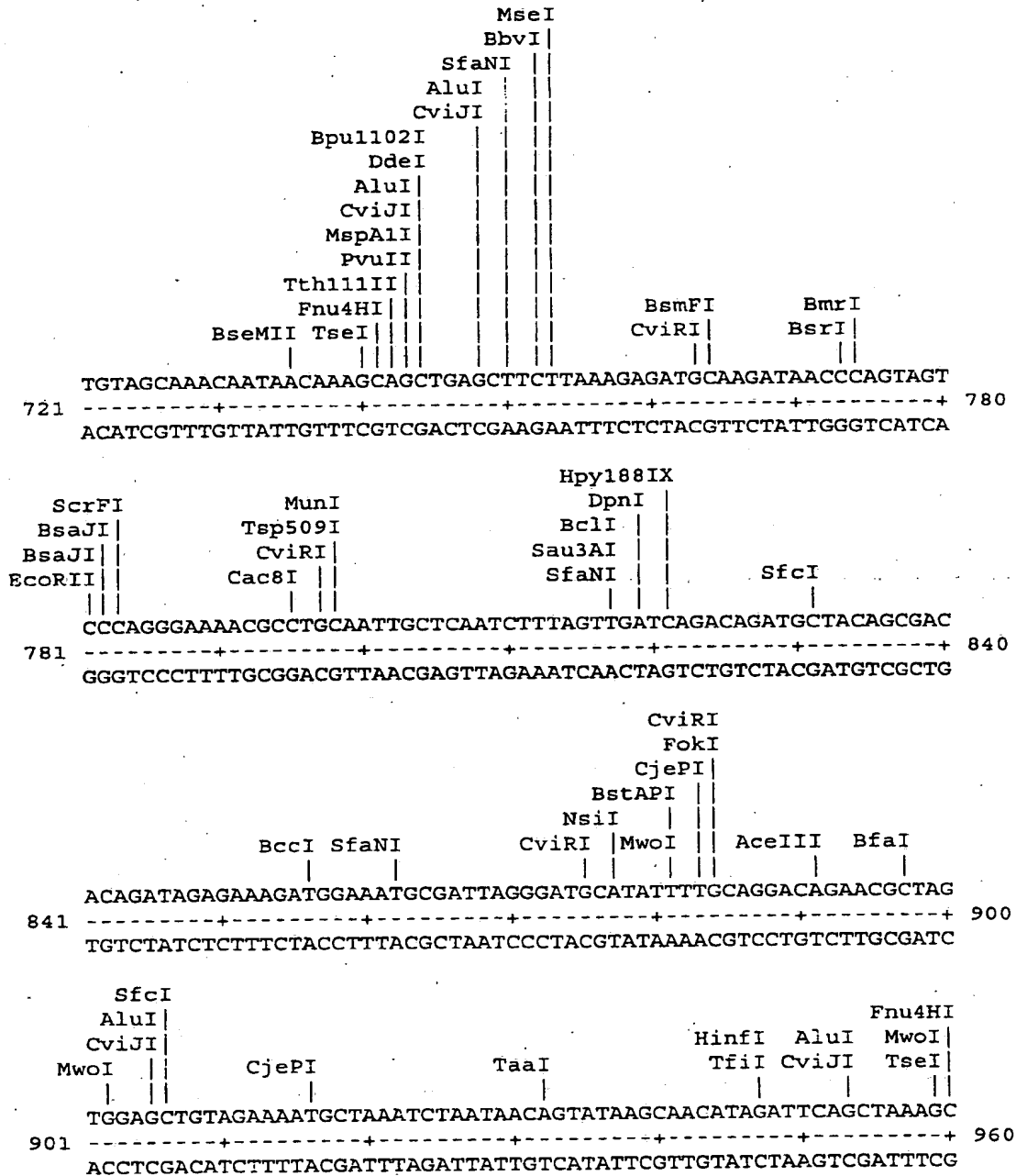
10044570.124404

Figure 2 (continued)



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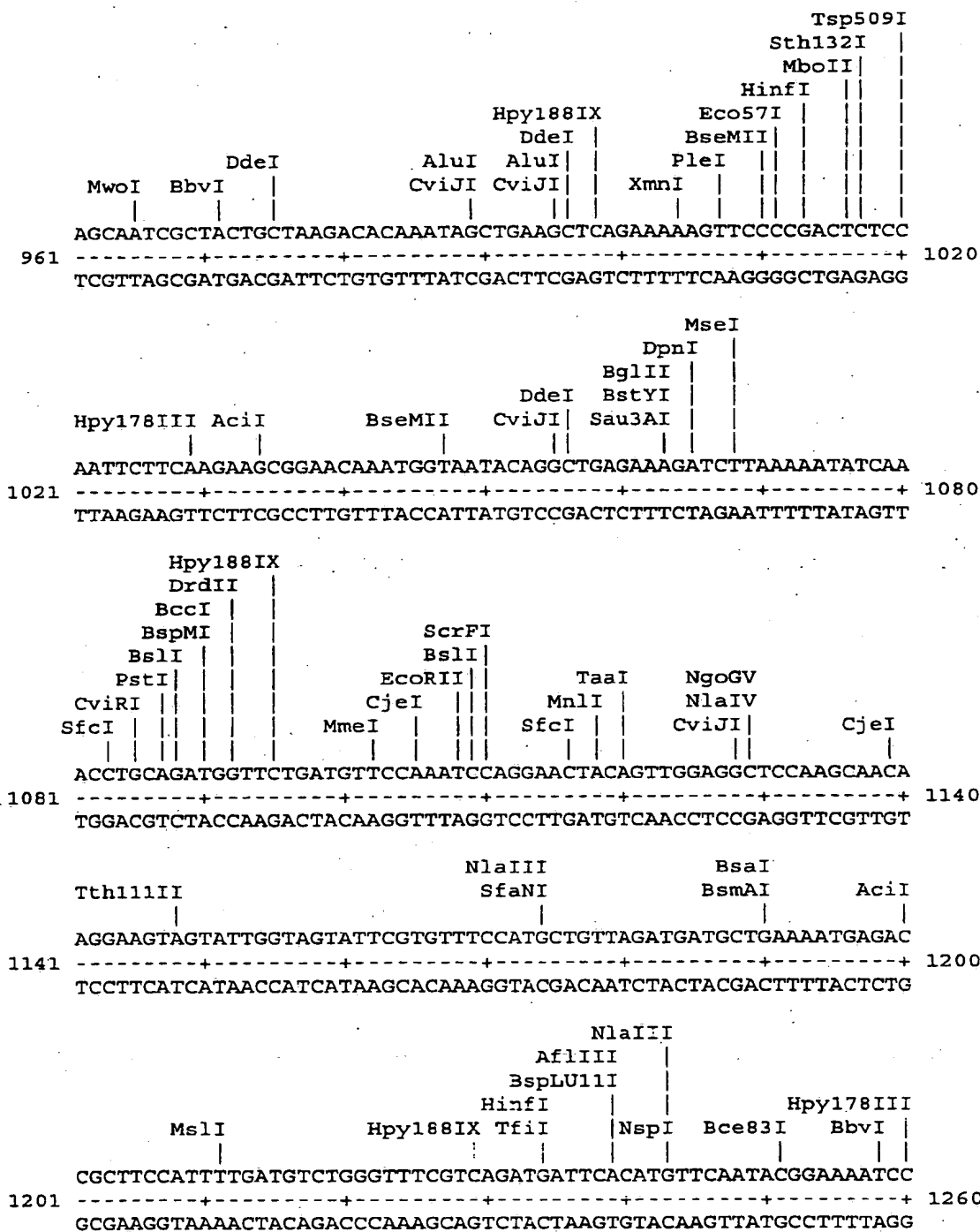
Figure 2 (continued)



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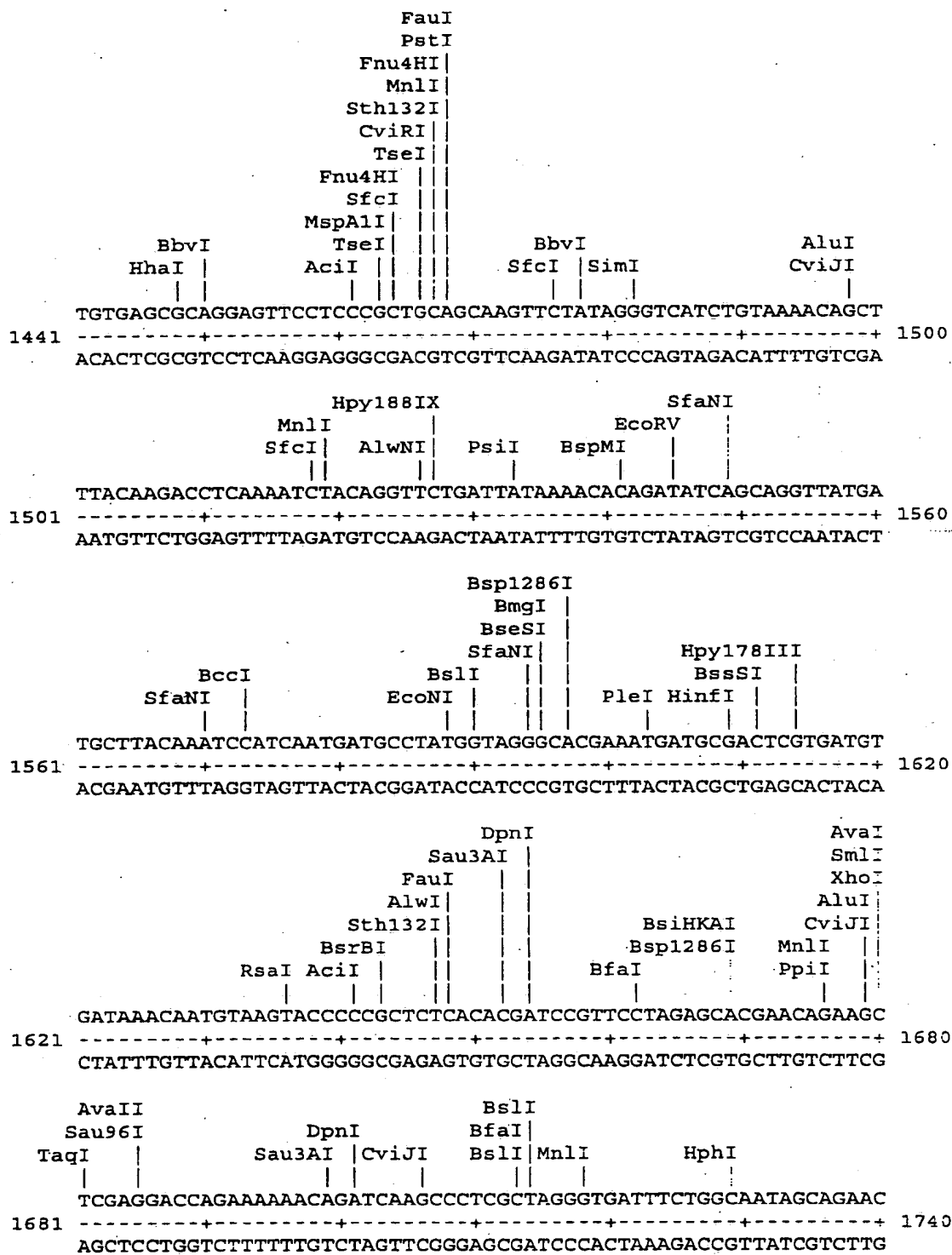
Figure 2 (continued)



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[illegible]

Figure 2 (continued)



10014670-121401

Figure 2 (continued)

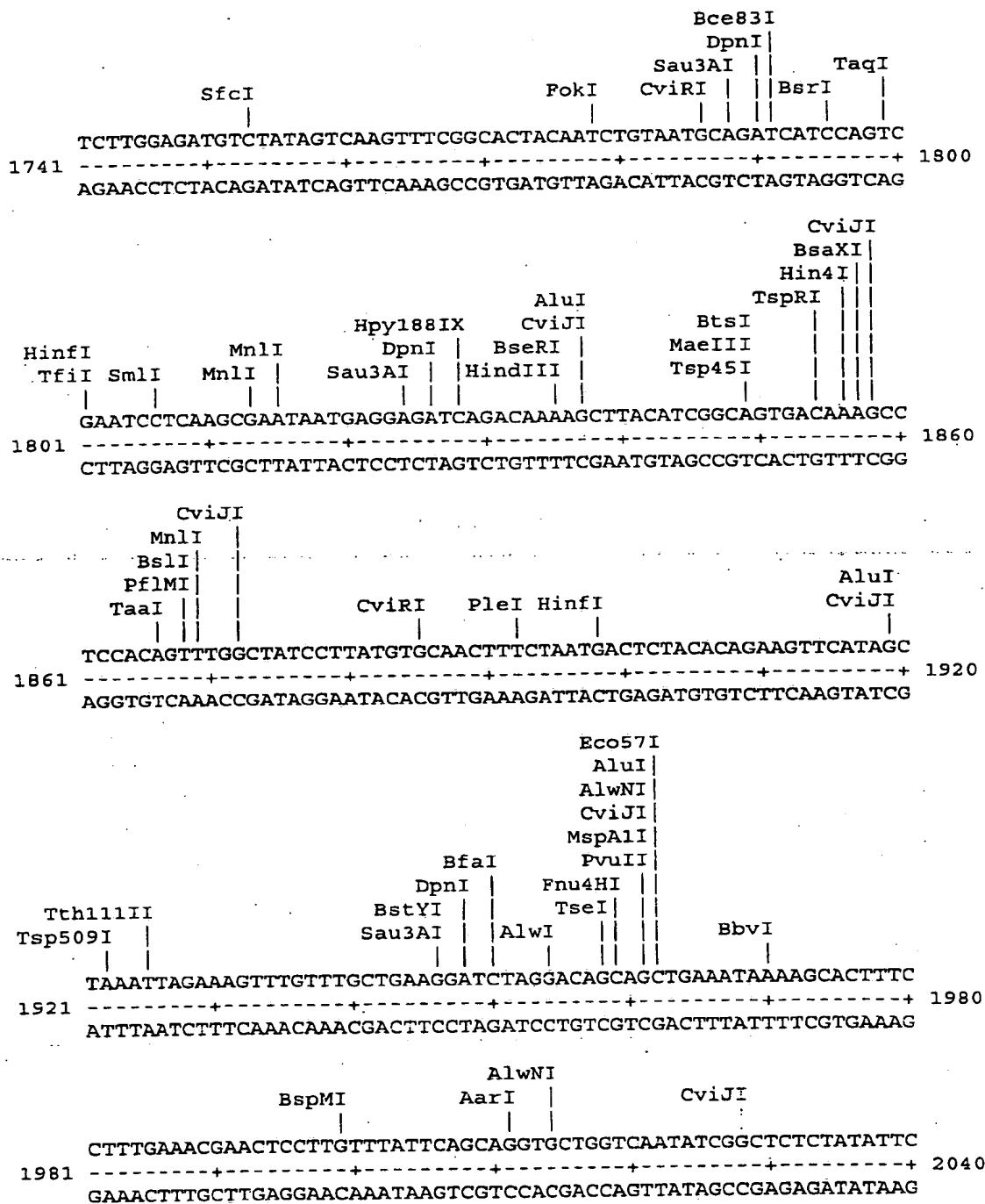
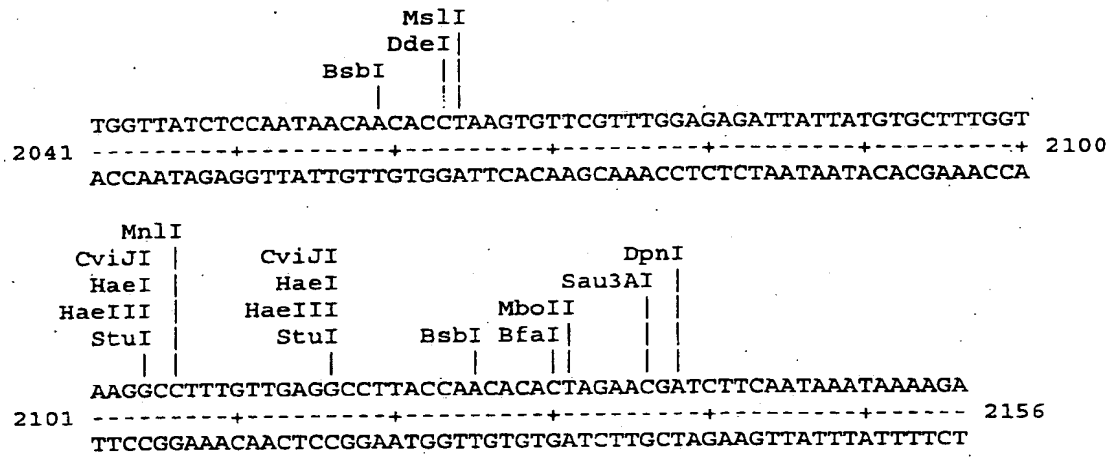


Figure 2 (continued)



10014570-121401

atgacaaaaa	aacattatgc	ttgggttgta	gaagggattc	tcaatcgttt	gcctaaacag	60
ttttttgtga	aatgtagtgt	tgtcgactgg	aacacattcg	ttccttcaga	aacctccact	120
acagaaaaag	ctgctacaaa	cgctatgaaa	tacaaatact	gtgtttggca	gtggctcgtc	180
ggaaagcata	gtcaggttcc	ttggatcaat	ggacagaaaa	agcctctata	tctttatgga	240
gctttcttaa	tgaacccttt	agcaaaggct	acgaagacta	cgttaaatgg	aaaagaaaac	300
ctagcttggt	ttattggagg	aactttaggg	ggactcagaa	aagctggaga	ctggctctgcc	360
acagtacggt	atgagtatgt	cgaagccttg	tcggttcag	aaatagatgt	ttcagggatt	420
ggccgtggta	at ttattaaa	gttttggttc	gcccaagcaa	ttgctgctaa	ctatgatcct	480
aaagaggcta	atgggttttac	aaattataaa	ggattttccg	ctctatatat	gtatggcatc	540
acagattctc	tatcattcag	agcttatggg	gcttactcca	aaccagcaaa	cgataaactc	600
ggcagtgatt	ttactttccg	aaagtttgat	ctaggtataa	tttcagcggt	<u>tt</u> aagtcaaa	660
ttttaataaaa	atcttttaaaa	acaggctcgc	attaattatt	agtgagagct	ttttttttat	720
tttttataat	aaaactaaaa	gattttttatt	at ttttttgag	ttttt atg gtt aat cct		777
				Met Val Asn Pro		
				1		
att ggt cca ggt cct ata gac gaa aca gaa cgc	aca cct ccc gca gat	825				
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg	Thr Pro Pro Ala Asp					
5 10 15 20						
ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa	873					
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu						
25 30 35						
gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc	921					
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr						
40 45 50						
gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc	969					
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu						
55 60 65						
atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct	1017					
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser						
70 75 80						
tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct	1065					
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro						
85 90 95 100						

Figure 3 (continued)

acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca	1113
Thr Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr	
105 110 115	
gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct	1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala	
120 125 130	
gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg	1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala	
135 140 145	
gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat	1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn	
150 155 160	
gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat	1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr	
165 170 175 180	
gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc	1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser	
185 190 195	
ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac	1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn	
200 205 210	
aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca	1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro	
215 220 225	
ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct	1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala	
230 235 240	
aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat	1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr	
245 250 255 260	
ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat	1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn	
265 270 275	
aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct	1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala	
280 285 290	
aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att	1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile	
295 300 305	

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Figure 3 (continued)

ctt	caa	gaa	gcg	gaa	caa	atg	gta	ata	cag	gct	gag	aaa	gat	ctt	aaa	1737
Leu	Gln	Glu	Ala	Glu	Gln	Met	Val	Ile	Gln	Ala	Glu	Lys	Asp	Leu	Lys	
	310					315					320					
aat	atc	aaa	cct	gca	gat	ggg	tct	gat	gtt	cca	aat	cca	gga	act	aca	1785
Asn	Ile	Lys	Pro	Ala	Asp	Gly	Ser	Asp	Val	Pro	Asn	Pro	Gly	Thr	Thr	
	325					330				335					340	
gtt	gga	ggc	tcc	aag	caa	caa	gga	agt	agt	att	ggc	agt	att	cgt	gtt	1833
Val	Gly	Gly	Ser	Lys	Gln	Gln	Gly	Ser	Ser	Ile	Gly	Ser	Ile	Arg	Val	
				345					350					355		
tcc	atg	ctg	tta	gat	gat	gct	gaa	aat	gag	acc	gct	tcc	att	ttg	atg	1881
Ser	Met	Leu	Leu	Asp	Asp	Ala	Glu	Asn	Glu	Thr	Ala	Ser	Ile	Leu	Met	
			360					365					370			
tct	ggg	ttt	cgt	cag	atg	att	cac	atg	ttc	aat	acg	gaa	aat	cct	gat	1929
Ser	Gly	Phe	Arg	Gln	Met	Ile	His	Met	Phe	Asn	Thr	Glu	Asn	Pro	Asp	
	375						380					385				
tct	caa	gct	gcc	caa	cag	gag	ctc	gca	gca	caa	gct	aga	gca	gcg	aaa	1977
Ser	Gln	Ala	Ala	Gln	Gln	Glu	Leu	Ala	Ala	Gln	Ala	Arg	Ala	Ala	Lys	
	390					395					400					
gcc	gct	gga	gat	gac	agt	gct	gct	gca	gcg	ctg	gca	gat	gct	cag	aaa	2025
Ala	Ala	Gly	Asp	Asp	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Asp	Ala	Gln	Lys	
	405					410				415				420		
gct	tta	gaa	gcg	gct	cta	ggg	aaa	gct	ggg	caa	caa	cag	ggc	ata	ctc	2073
Ala	Leu	Glu	Ala	Ala	Leu	Gly	Lys	Ala	Gly	Gln	Gln	Gln	Gly	Ile	Leu	
				425					430					435		
aat	gct	tta	gga	cag	atc	gct	tct	gct	gct	gtt	gtg	agc	gca	gga	gta	2121
Asn	Ala	Leu	Gly	Gln	Ile	Ala	Ser	Ala	Ala	Val	Val	Ser	Ala	Gly	Val	
			440					445					450			
ctc	ccg	ctg	cag	caa	gtt	cta	tgg	atc	cga	gct	cgg	tac	caa	gct	tac	2169
Leu	Pro	Leu	Gln	Gln	Val	Leu	Trp	Ile	Arg	Ala	Arg	Tyr	Gln	Ala	Tyr	
			455				460					465				
gta	gaa	caa	aaa	ctc	atc	tca	gaa	gag	gat	ctg	aat	agc	gcc	gtc	gac	2217
Val	Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Ser	Ala	Val	Asp	
	470					475					480					
cat	cat	cat	cat	cat	cat	tga										2238
His	His	His	His	His	His											
	485				490											

10014670-121401

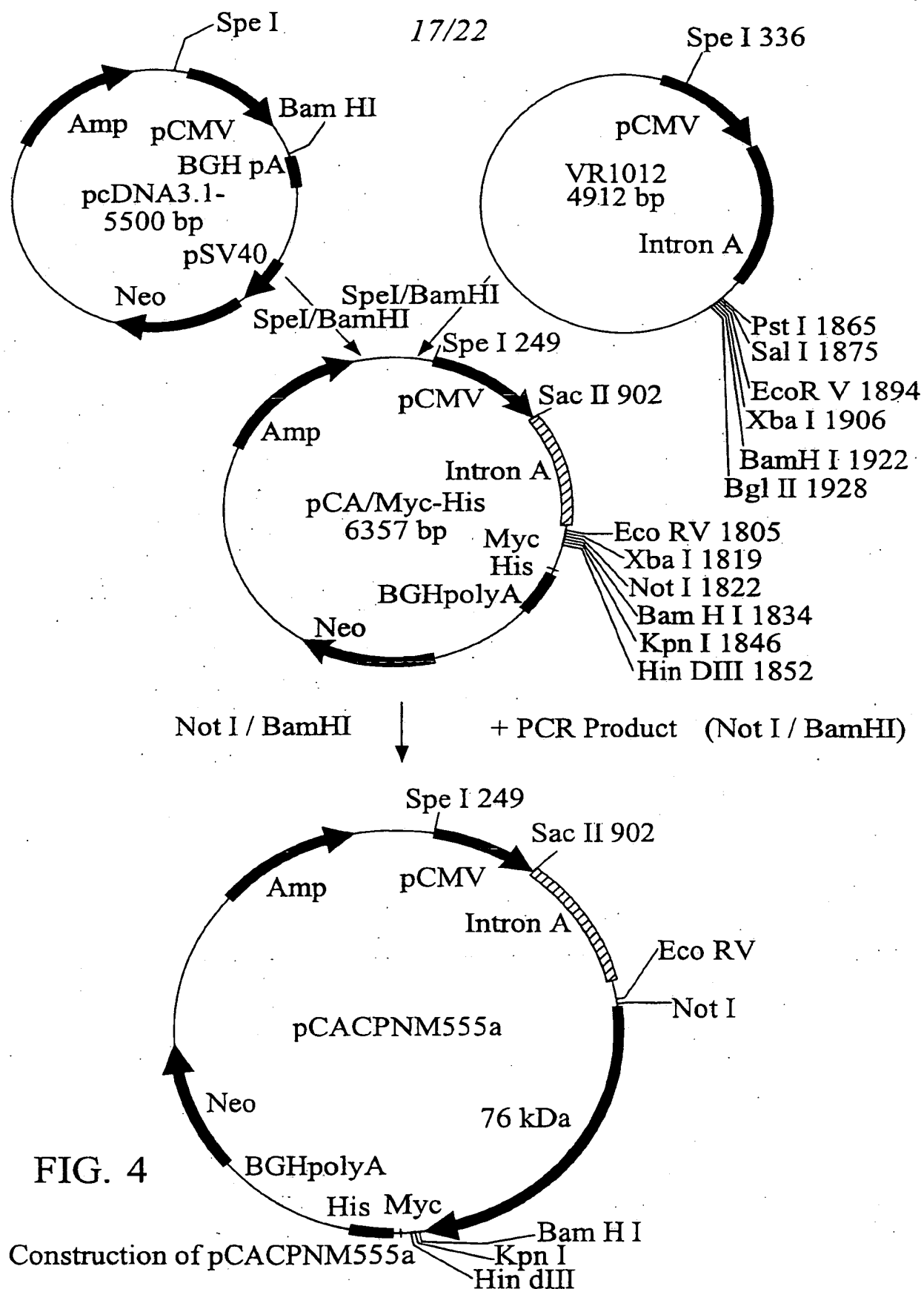


FIG. 4

Construction of pCACPNM555a

10014670-121401

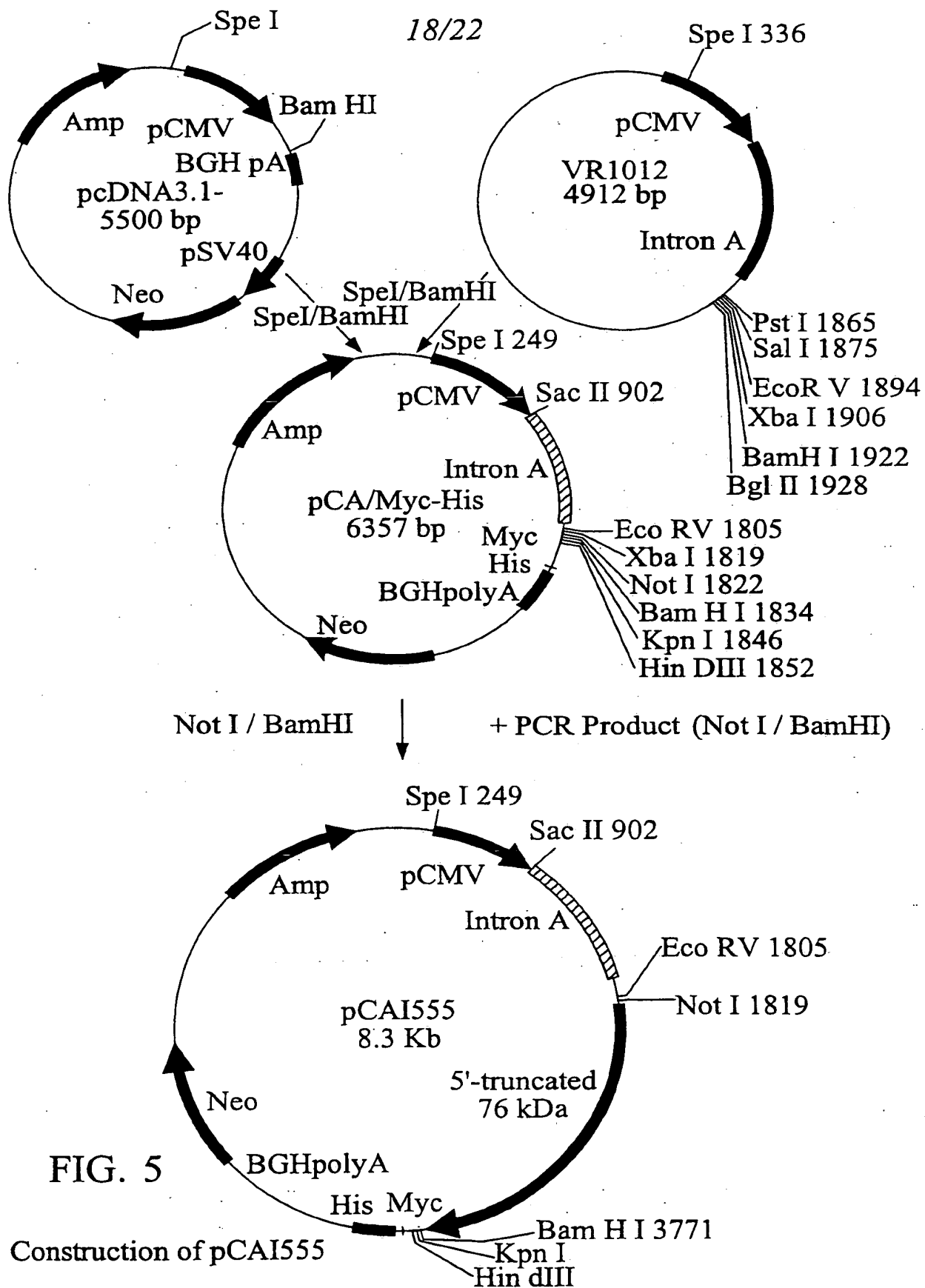


FIG. 5

Construction of pCAI555

10014670-121401

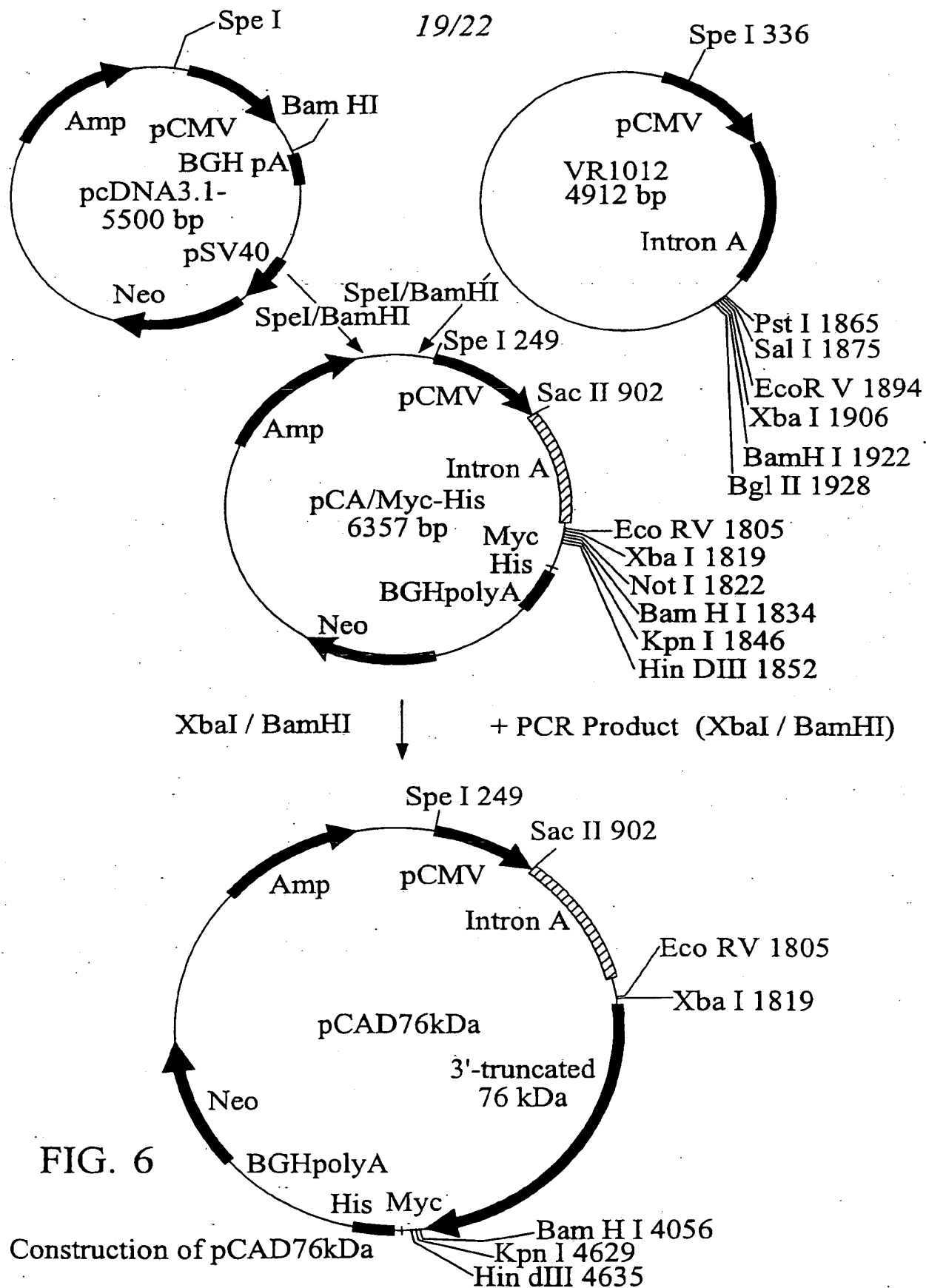


FIG. 6

Construction of pCAD76kDa

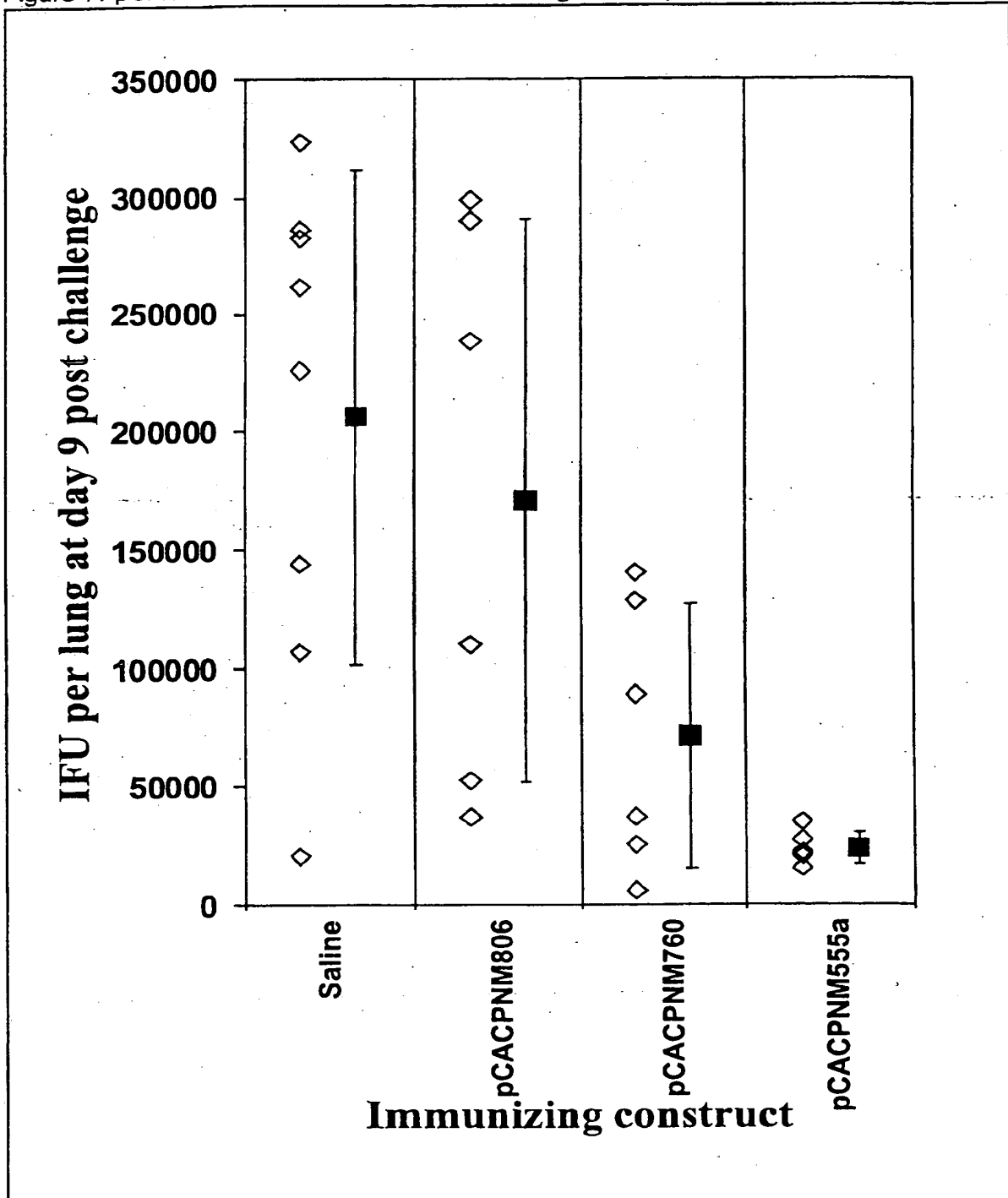
Figure 7: pCACPNM555a Confers Protection Against *C. pneumoniae* Infection .

Figure 8: pCAI555 Confers Protection Against *C. pneumoniae* Infection.

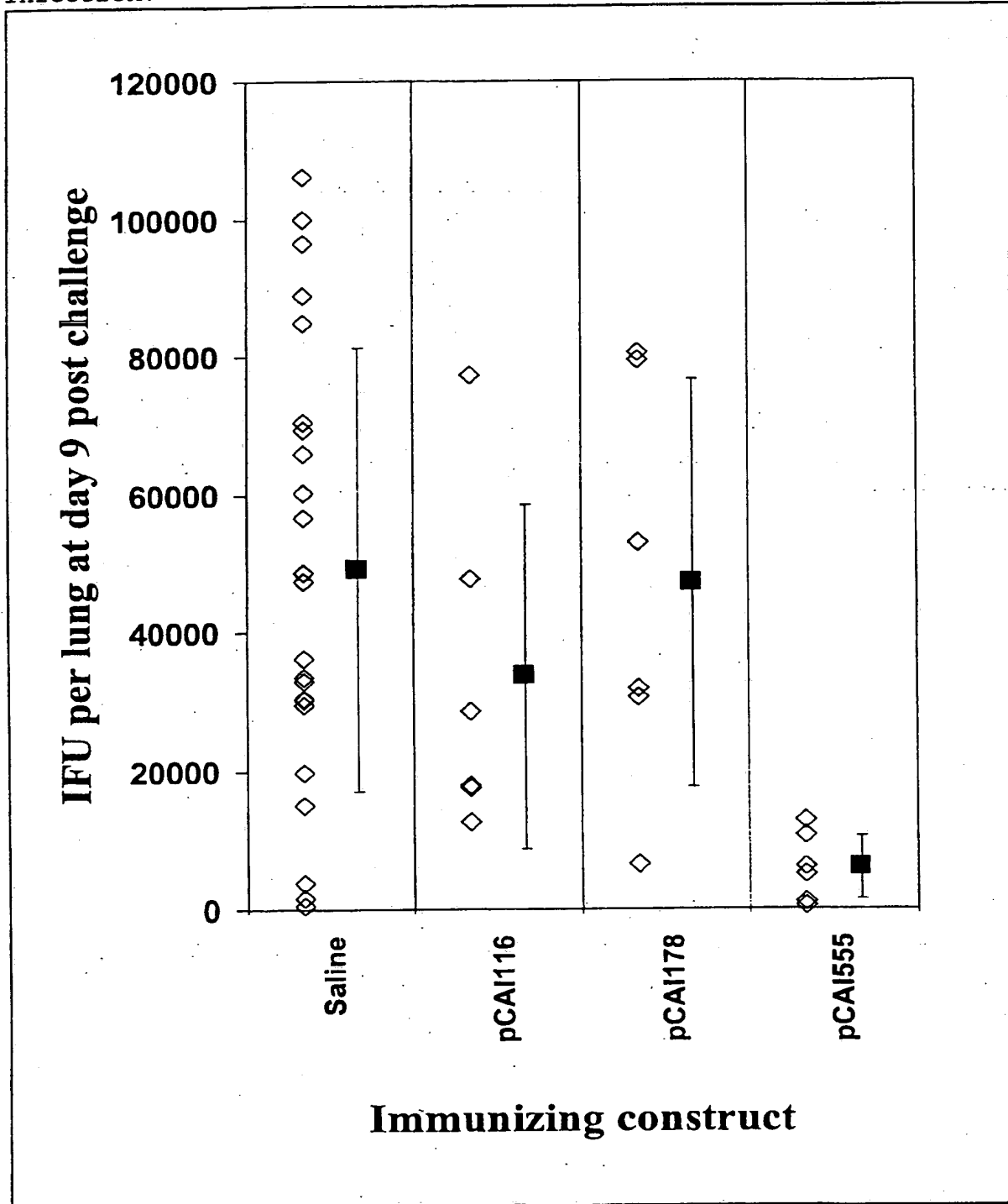


Figure 9: pCAD76kDa Confers Protection against *C. pneumoniae* Infection.

